Bril

## **RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

10/539, 032
PCT
06/22/2005

## ENTERED



PCT

RAW SEQUENCE LISTING DATE: 06/22/2005 PATENT APPLICATION: US/10/539,032 TIME: 10:30:27

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\06222005\J539032.raw

```
3 <110> APPLICANT: JAPAN SCIENCE AND TECHNOLOGY AGENCY
     5 <120> TITLE OF INVENTION: Glucose and/or fructose transporter 'NaGLT1' and gene
     7 <130> FILE REFERENCE: 4439-4034
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/539,032
C--> 10 <141> CURRENT FILING DATE: 2005-06-13
     12 <150> PRIOR APPLICATION NUMBER: JP P2002-363014
    13 <151> PRIOR FILING DATE: 2002-12-13
    15 <160> NUMBER OF SEQ ID NOS: 30
    17 <170> SOFTWARE: PatentIn Ver. 2.1
    19 <210> SEQ ID NO: 1
    20 <211> LENGTH: 2173
    21 <212> TYPE: DNA
    22 <213> ORGANISM: Rattus norvegicus
    24 <220> FEATURE:
    25 <221> NAME/KEY: CDS
    26 <222> LOCATION: (111) .. (1562)
    28 <400> SEQUENCE: 1
    29 aaagaatett etggttagaa agaaetgggg eteagagete eagggaeeet ggeaaaaage 60
    31 tggacctcac caaaaaccct ttgtctggag ccaccaagct ggggtcggaa atg gag
    32
                                                                Met Glu
    33
    35 ttc cgt ggg tcc ggg gcc act gct gtt gag cag cac ctc ctc cag tcc
                                                                           164
    36 Phe Arg Gly Ser Gly Ala Thr Ala Val Glu Gln His Leu Leu Gln Ser
    39 gag acc cca ggg aag aat ggg ctg cag gcc aca tcg agt gac caa gtg
                                                                           212
    40 Glu Thr Pro Gly Lys Asn Gly Leu Gln Ala Thr Ser Ser Asp Gln Val
                                 25
    43 gga aga aca ctg cgc tgg ttc acc act gtg gtt ctg aat gct gct ttc
                                                                           260
    44 Gly Arg Thr Leu Arg Trp Phe Thr Thr Val Val Leu Asn Ala Ala Phe
                             40
                                                 45
    47 ctg gga atg gga gtg agc gct gct gtg ctg gga ccc aca ttt cca gac
    48 Leu Gly Met Gly Val Ser Ala Ala Val Leu Gly Pro Thr Phe Pro Asp
    49
                         55
                                             60
    51 ctg gcc aga aac gtg aac cgg aac atc agc agc ctt tcc gaa atc ttc
                                                                           356
    52 Leu Ala Arg Asn Val Asn Arg Asn Ile Ser Ser Leu Ser Glu Ile Phe
                                         75
    55 gtg ggc cga gcc ctc ggc tac ctg ggc ggc tct gtg gtt ggt ggg gtg
                                                                           404
    56 Val Gly Arg Ala Leu Gly Tyr Leu Gly Gly Ser Val Val Gly Gly Val
                                     90
    59 ctt ttc gac tgc atg aat cat ttt cta ctt ttg ggg ctg tcc cac ctg
                                                                           452
    60 Leu Phe Asp Cys Met Asn His Phe Leu Leu Leu Gly Leu Ser His Leu
           100
                                105
    63 ctt act gcg gcc ggt ctt tac ctc act cct ttc tgt aaa aca gct gcc
                                                                           500
```

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\06222005\J539032.raw

		Thr	Ala	Ala	Gly		Tyr	Leu	Thr	Pro		Cys	Lys	Thr	Ala	Ala	
	115					120					125					130	
				gcc		_					_				_	_	548
68	Leu	Leu	Thr	Ala	Met	Met	Ser	Ile	Thr	Gly	Val	Ser	Phe	Gly	Val	Leu	
69					135					140					145		
				ggg													596
	Asp	Thr	Gly	Gly	Asn	Val	Leu	Ile	Leu	Asp	Leu	Trp	Gly	Asp	Lys	Gly	
73				150					155					160			
				att													644
76	Ala	Pro	His	Ile	Gln	Ala	Leu	His	Phe	Ser	Phe	Ala	Leu	Gly	Ala	Phe	
77			165					170					175				
				ctg													692
80	Leu		Pro	Leu	Leu	Ala	Lys	Leu	Ala	Trp	Gly	Thr	Thr	Ala	Ser	Ala	
81		180					185					190					
				aca													740
		Asn	His	Thr	Glu	Pro	Gln	Leu	Asp	Arg	Ser	Ala	Leu	Asn	Arg	Ser	
	195					200					205					210	
				gcc													788
	Phe	Glu	Ala	Ala		Asp	Ser	Val	Leu		Val	Pro	Asp	Asp		Asn	
89					215					220					225		
				gcg													836
	Leu	Leu	$\mathtt{Trp}$	Ala	$\mathtt{Tyr}$	Ala	Ser	Ile		Thr	Tyr	Val	Leu	Val	Leu	Ser	
93				230					235					240			
				ttt													884
	Val	Phe		Phe	Ala	Pro	Phe		Lys	Lys	Arg	Ser	-	Gln	Lys	Lys	
97			245					250					255				
				tct													932
				a Ser	Ala	Glr	_		Arg	g Arg	g Ala	_	_	His	s Arg	g Ala	
101		260					265					270					
																gag	980
			Cys	s Leu	Let			Phe	Phe	Phe			· Val	. GI	Ala	Glu	
	275					280					285					290	
											-				_	ggc	1028
		Thr	Туг	GIY		_	Val	Phe	Ser			Thr	Thr	His		lGly	
109					295					300					305		
																g acc	1076
		GIU	GIU			ı Ala	. Ala	GLY			ı Ser	: IIe	Pne	_	_	Thr	
113				310					315					320			
115	י דנט	gca	ged	tgo	agg	ggo	ctg	gcc	ato	: דנכ	: דנכ	: gca	ı acg	ctc	: tta	a cag	1124
		Ala			Arg	GIY	ьeu			Pne	Pne	AT8			і ьеі	ı Gln	
117			325					330					335				
																tct	1172
				. Met	мес	. vai		_	ASI	1 116	e GIA			ALō	sei	Ser	
121		340		. ~			345					350				<b>.</b>	1000
																gcg	1220
			: цет	ı val	ьeu		_	туѕ	ser	Pro		_	ь тел	ırr	) TTE	Ala	
	355			. +	~~-	360			. ~~+	. ~~-	365		~~-			370	1000
																atc	1268
126	ser	ser	val	. ıyr	GTĀ	ATA	ser	met	мта	r ATS	unr	. rue	Pro	ser	. GT.	/ Ile	

Input Set: A:\Sequence Listing.txt
Output Set: N:\CRF4\06222005\J539032.raw

129					375					380					385					
131	tcc	tgg	att	gag	cag	tac	acc	acc	tta	act	ggg	aaa	tcc	qct	qcq	ttc	1316			
		Trp																		
133		_		390		-			395		_	_		400						
135	att	ctg	gtt	ggt	gct	gcc	ctg	gga	cta	atg	gcg	act	cct	gca	tta	tct	1364			
136	Ile	Leu	Val	Gly	Ala	Ala	Leu	Gly	Leu	Met	Ala	Thr	Pro	Āla	Leu	Ser				
137			405					410					415							
139	gga	att	ctt	cag	gga	cac	tat	ccc	gat	ctg	cca	gta	att	ctg	tac	atg	1412			
140	Gly	Ile	Leu	Gln	Gly	His	Tyr	Pro	Asp	Leu	Pro	Val	Ile	Leu	Tyr	Met				
141		420					425		_			430			_					
143	tgt	ctg	ggc	tca	gca	gta	tta	aca	act	gtg	tta	ttc	cct	gtg	atg	tat	1460			
144	Cys	Leu	Gly	Ser	Ala	Val	Leu	Thr	Thr	Val	Leu	Phe	Pro	Val	Met	Tyr				
145	435					440					445					450				
147	aaa	gta	gcc	acc	tta	cct	ctg	gat	cga	aag	cag	gaa	aaa	agc	atc	aac	1508			
		Val	_				_	_	_	_	_	_		_						
149	_				455			_	_	460			_		465					
151	agt	gag	ggc	cag	aaa	ata	tta	ctt	tct	agc	tct	agg	cta	atc	aag	gaa	1556			
		Glu																		
153				470					475			_		480	_					
155	gct	aaa	tgaa	agag	gga a	agggg	gaaag	gg to	gtgaa	aagca	a cgt	tgcg	gcg	tgt	gtgc	gca	1612			
	Ala								_	_										
158	tgca	acgcg	gca d	gcgt	aat	gg tt	ttg	ggt	g gti	taaaa	atga	agaa	atgg	gac a	attct	ctaat	1672			
160	aaaa	aatao	caa t	agaa	aatgo	cc tt	tata	ataad	c cca	atago	ctga	ggto	ctcta	aag o	caact	ctcct	1732			
162	gaaa	atatt	ct g	gcago	cag	gg to	cttct	ccag	g ct	O aaaaatacaa tagaaatgoo tttatataac ccatagotga ggtototaag caactotoot 2 gaaatattot goagocaggg tottotocag otgacaggga goacgoagto atgaggoaco										
164	aggt	tctcc	ctg a	agaco	cctt	ca ca	actgo	cct	att		gtta	tct	ctca	gcc (	catga	attcta				
										tgaag							1852			
166	ggaa	aagaa	aaa g	gtatt	tcta	aa aa	ataaa	aatc	ace	tgaag gactt	cca	gaga	atcci	gt a	aagad	attcta	1852 1912			
166 168	ggaa tgag	aagaa gagat	aaa g	gtatt atgta	tcta	aa aa ge ea	ataaa agcad	atco	c acq	tgaag gactt cattt	cca	gaga tgaa	atcci agtga	gt a	aagad	attcta cagctc gaacag	1852 1912 1972			
166 168 170	ggaa tgag aaat	aagaa gagat tagtt	aaa g ca a tt a	gtatt atgta aaacg	tcta acto gtato	aa aa go ca go to	ataaa agcad cctgg	aatco cctto gggct	acg tto	tgaag gactt cattt tgaga	cca cca atgg	gaga tgaa ctta	atcci agtga agtga	igt a aga d gtt a	aagad cacag aagag	attcta cagctc	1852 1912 1972 2032			
166 168 170 172	ggaa tgag aaat actg	aagaa gagat tagtt gctct	aaa g ca a tt a	gtatt atgta aaacg caaag	tcta acto gtato ggtco	aa aa ge ea ge to et ga	ataaa agcad cctgg agtto	aatco cctto gggct caaat	acq tto ggt	tgaag gactt cattt tgaga cagca	cca cca atgg aacc	gaga tgaa ctta acat	atcci agtga agtga agtg	igt a aga d gtt a ggc t	aagad cacag aagag ccaca	attota cagoto gaacag gcactg	1852 1912 1972 2032 2092			
166 168 170 172 174	ggaa tgag aaat actg	aagaa gagat tagtt gctct	aaa g ca a tt a tc d gag a	gtatt atgta aaacg aaaag atctg	tcta acto gtato ggtco gatgo	aa aa go ca go to ot ga co tt	ataaa agcad cctgg agtto	aatco cctto gggct caaat	acq tto ggt	tgaag gactt cattt tgaga cagca	cca cca atgg aacc	gaga tgaa ctta acat	atcci agtga agtga agtg	igt a aga d gtt a ggc t	aagad cacag aagag ccaca	attota cagoto gaacag gcactg aactat	1852 1912 1972 2032 2092			
166 168 170 172 174 176	ggaa tgag aaat actg ctgt	aagaa gagat tagtt gctct taatg	taa g tt a tt o gag a	gtatt atgta aaacg caaag atctg aaata	tcta acto gtato gatoo gatoo aatao	aa aa ge ea ge to et ga ee tt	ataaa agcad cctgg agtto	aatco cctto gggct caaat	acq tto ggt	tgaag gactt cattt tgaga cagca	cca cca atgg aacc	gaga tgaa ctta acat	atcci agtga agtga agtg	igt a aga d gtt a ggc t	aagad cacag aagag ccaca	attota cagoto gaacag gcactg aactat	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 179	ggaa tgag aaat actg ctgt taca <210	aagaa gagat tagtt getet taatg atcaa	taa o tta a ttc o gag a tat a	gtatt atgta aaacg aaaag atctg aaata O NO:	tcta acto gtato gatgo gatgo aatat	aa aa ge ea ge to et ga ee tt	ataaa agcad cctgg agtto	aatco cctto gggct caaat	acq tto ggt	tgaag gactt cattt tgaga cagca	cca cca atgg aacc	gaga tgaa ctta acat	atcci agtga agtga agtg	igt a aga d gtt a ggc t	aagad cacag aagag ccaca	attota cagoto gaacag gcactg aactat	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 179 180	ggaa tgag aaat actg ctgt taca <210 <211	aagaa gagat tagtt getet taatg atcaa D> SE 1> LE 2> TY	aaa g tta a ttc o gag a aat a EQ II ENGTH	gtatt atgta aaacg atctg aaata O NO: 48 PRT	tcta aactg gtatg ggtco gatgo aatat 2	aa aa ge ea ge to get ga ee tt	ataaa agcac cctgg cctgg ccttc	aatoo eetto ggget caaat etggt	e ace e tto ggt e cce e gte	tgaag gactt cattt tgaga cagca	cca cca atgg aacc	gaga tgaa ctta acat	atcci agtga agtga agtg	igt a aga d gtt a ggc t	aagad cacag aagag ccaca	attota cagoto gaacag gcactg aactat	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 179 180	ggaa tgag aaat actg ctgt taca <210 <211	aagaa gagat tagtt getet taatg atcaa O> SE	aaa g tta a ttc o gag a aat a EQ II ENGTH	gtatt atgta aaacg atctg aaata O NO: 48 PRT	tcta aactg gtatg ggtco gatgo aatat 2	aa aa ge ea ge to get ga ee tt	ataaa agcac cctgg cctgg ccttc	aatoo eetto ggget caaat etggt	e ace e tto ggt e cce e gte	tgaag gactt cattt tgaga cagca	cca cca atgg aacc	gaga tgaa ctta acat	atcci agtga agtga agtg	igt a aga d gtt a ggc t	aagad cacag aagag ccaca	attota cagoto gaacag gcactg aactat	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 179 180 181 182 184	ggaa tgag aaat actg ctgt taca <210 <211 <213 <400	aagaa gagat tagtt gctct caat gatcaa tcaa	aaa g tt a tt c tt c gag a aat a EQ II ENGTH PE: RGANI	gtatt atgta aaacg atctg atatt NO: H: 48 PRT ESM:	tteta acto gtato ggtco gatgo actat 2 34 Ratt	aa aa ge ca ge to eet ga ee tt et t	ataaa agcac cctgo agtto cctto	aatco cctto gggct caaat ctggt	e acg e tto e ggt e cco e gto	tgaag gactt cattt tgaga cagca gtctg	cca cca atgg aacc gaag	gaga tgaa ctta acat acag	atcol agtga agtgo oggto goga	igt a aga o gtt a ggc t cag t	aagad aagad aagad ccaca	atteta cagete gaacag gcaetg aactat etcata	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 179 180 181 182 184	ggaa tgag aaat actg ctgt taca <210 <211 <213 <400	aagaa gagat tagtt getet taatg atcaa 0> SE 1> LE 2> TY 3> OF	aaa g tt a tt c tt c gag a aat a EQ II ENGTH PE: RGANI	gtatt atgta aaacg atctg atatt NO: H: 48 PRT ESM:	tteta acto gtato ggtco gatgo actat 2 34 Ratt	aa aa ge ca ge to eet ga ee tt et t	ataaa agcac cctgo agtto cctto	aatco cctto gggct caaat ctggt	e acg e tto e ggt e cco e gto	tgaag gactt cattt tgaga cagca gtctg	cca cca atgg aacc gaag	gaga tgaa ctta acat acag	atcol agtga agtgo oggto goga	igt a aga o gtt a ggc t cag t	aagad aagad aagad ccaca	atteta cagete gaacag gcaetg aactat etcata	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 179 180 181 182 184 185	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met	aagaa gagat tagtt getet taatgateaa 0> SE 1> LE 2> TY 3> OF Glu	aaa g tt a tt a tt c gag a aat a EQ II ENGTH YPE: CGANI Phe	gtatt atgta atagta aaacg atctg aaata D NO: H: 48 PRT ESM: ICE: Arg	tteta aacte gtate ggtee gatge aatat 2 34 Ratt 2 Gly	aa aa gc ca gc to cc t ga cc t t cus r	ataaa agcac cctg agtto cctto orve	aatcocctto gggct caaat ctggt	e ace to tto ggt c ccc gte	tgaag gactt cattt cgaga cagca gtctc	cca cca atgg aacc gaag	gaga tgaa ctta acat acag	atco agtga agtg gggt gcga	gt a aga o gtt a ggc t cag t	Leu 15	attota cagoto gaacag gcactg aactat ctcata	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 179 180 181 182 184 185 186	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met	aagaa gagat tagtt gctct caat gatcaa tcaa	aaa g tt a tt a tt c gag a aat a EQ II ENGTH YPE: CGANI Phe	gtatt atgta atagta aaacg atctg aaata D NO: H: 48 PRT ESM: ICE: Arg	tteta aacte gtate ggtee gatge aatat 2 34 Ratt 2 Gly	aa aa gc ca gc to cc t ga cc t t cus r	ataaa agcac cctg agtto cctto orve	aatcocctto gggct caaat ctggt	e ace to tto ggt c ccc gte	tgaag gactt cattt cgaga cagca gtctc	cca cca atgg aacc gaag	gaga tgaa ctta acat acag	atco agtga agtg gggt gcga	gt a aga o gtt a ggc t cag t	Leu 15	attota cagoto gaacag gcactg aactat ctcata	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 179 180 181 182 184 185	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met	aagaa gagat tagtt getet taatgateaa 0> SE 1> LE 2> TY 3> OF Glu	aaa g tt a tt a tt c gag a aat a EQ II ENGTH YPE: CGANI Phe	gtatt atgta aaacg atcto aaata D NO: H: 48 PRT SM: JCE: Arg	tteta acto getec gatgo actal 2 Ratt 2 Gly Pro	aa aa gc ca gc to cc t ga cc t t cus r	ataaa agcac cctgo agtto cctto Gly Lys	aatcoccttogggctcaaatctggt	e ace tto ggt c ccc gts  Thr	egaag gactt cattt cgaga cagca gtcts Ala 10 Leu	cca cca atgg aacc gaag Val	gaga tgaa ctta acat acat acat	atco agtga agtg gggt gcga Gln	gt agga oggt agge tragge tragge tragge tragget	Leu 15 Ser	attota cagoto gaacag gcactg aactat ctcata	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 179 180 181 182 184 185 186 188	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met 1 Gln	aagaa gagat tagtt getet taatgateaa 0> SE 1> LE 2> TY 3> OF Glu	aaa o ca a ctc o gag a aat a EQ II ENGTH PE: CGANI Phe	gtatt atgta aaacg atcto aaata D NO: H: 48 PRT SM: ICE: Arg	tteta acte gtate gatgo actat 2 Ratt 2 Gly Pro	aa aa gc ca gc to gc to gc to tc t t	ataaa agcac cctgo agtto cctto Gly Lys	aatcoccttogggctcaaatctggt	tace tto ggt cocc gto	Ala Leu	cca cca atgg aacc gaag Val	gaga tgaa ctta acat acat acat	atco agtga agtga ggga Gln	tgt a aga o gtt a ggc t cag t His Ser 30	Leu 15 Ser	attota cagoto gaacag gcactg actat ctcata  Leu Asp	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 179 180 181 182 184 185 188 189 191	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met 1 Gln	aagaa gagat tagtt gctct caatcaa D> SE 1> LE 2> TY 3> OF Glu Ser Val	aaa caaa caaa caaa caaa caaa caaa caaa	gtatt atgta aaacg atctg aaata D NO: H: 48 PRT SSM: NCE: Arg Thr 20 Arg	ttcta actorized gtatorized gatgorized actati 2 Ratti 2 Gly 5 Pro	aa aa gc ca gc to gc to gc to gc tt tt t	ataaa agcad cctgg agtto cctto Gly Lys Arg	aatcocctto	c ace tto ggt c ccc gto	Ala 10 Leu	cca cca atgg aacc gaag Val Gln	gaga tgaa ctta acat acat acat acat val	atcomagtgagtgagtgggadGln Thr Val	His Ser 30 Leu	Leu 15 Ser Asn	attota cagoto gaacag goactg actat ctcata  Leu Asp	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 180 181 182 184 185 186 188 191 192 194	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met 1 Gln	aagaa gagat tagtt tagtt taatcaa 0> SE 1> LE 2> TY 3> OF Glu Ser	aaa caaa caaa caaa caaa caaa caaa caaa	gtatt atgta aaacg atctg aaata D NO: H: 48 PRT SSM: NCE: Arg Thr 20 Arg	ttcta actorized gtatorized gatgorized actati 2 Ratti 2 Gly 5 Pro	aa aa gc ca gc to gc to gc to gc tt tt t	ataaa agcad cctgg agtto cctto Gly Lys Arg	aatcocctto	c ace tto ggt c ccc gto	Ala 10 Leu	cca cca atgg aacc gaag Val Gln	gaga tgaa ctta acat acat acat acat val	atcomagtgagtgagtgggadGln Thr Val	His Ser 30 Leu	Leu 15 Ser Asn	attota cagoto gaacag goactg actat ctcata  Leu Asp	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 180 181 182 184 185 186 188 191 192 194 195	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met 1 Gln Ala	aagaa gagat tagtt gctct caatcaa 0> SE 1> LE 2> TY 3> OF Glu Ser Val	aaa caaa caaca caa	gtatt atgta aaacg atcto aaata D NO: H: 48 PRT SSM: NCE: Arg Thr 20 Arg	gtateggtateggatatateggatatateggatateg	aa	ataaa agcad cctgg agtto cctto Oorve Gly Lys Arg Val	egicu Ala Asn Trp 40 Ser	c ace tto ggt c ccc gto	Ala 10 Leu Thr	val Thr	Glu Ala Val Leu 60	Gln Val Gly	His Ser 30 Leu Pro	Leu 15 Ser Asn	Leu Asp Ala Phe	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 180 181 182 184 185 186 188 191 192 194 195	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met 1 Gln Ala Pro	aagaa gagat tagtt gctct caatcaa O> SE 1> LE 2> TY 3> OF Glu Ser Val	aaa caaa caaca caa	gtatt atgta aaacg atcto aaata D NO: H: 48 PRT SSM: NCE: Arg Thr 20 Arg	gtateggtateggatatateggatatateggatateg	aa	ataaa agcad cctgg agtto cctto Oorve Gly Lys Arg Val	egicu Ala Asn Trp 40 Ser	c ace tto ggt c ccc gto	Ala 10 Leu Thr	val Thr	Glu Ala Val Leu 60	Gln Val Gly	His Ser 30 Leu Pro	Leu 15 Ser Asn	Leu Asp Ala Phe	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 180 181 182 184 185 186 188 191 192 194 195 197	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met 1 Gln Ala Pro 65	aagaa gagat tagtt tagtt gctct taatcaa 0> SE 1> LE 2> TY 3> OF 0> SF Glu Ser Val Phe 50 Asp	aaa caa caa caa caa caa caa caa caa caa	gtatt atgta aaacg atctg aaata O NO: H: 48 PRT SSM: JCE: Arg Thr 20 Arg Gly	ttcta actorized gtatorized gatgorized actatorized acta	aa	ataaa agcac cctgg agtto cctto Gly Lys Arg Val 55	egicu Ala Asn Trp 40 Ser Asn	c ace the ggt c ccc gte Thr Gly 25 Phe Ala	Ala 10 Leu Thr Ala Asn	Val Gln Thr Val Ile	Glu Ala Val Leu 60 Ser	Gln Thr Val 45 Gly Ser	His Ser 30 Leu Pro	Leu 15 Ser Asn	Leu Asp Ala Phe Glu 80	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 180 181 182 184 185 186 188 191 192 194 195 197 198 200	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met 1 Gln Ala Pro 65	aagaa gagat tagtt gctct caatcaa 0> SE 1> LE 2> TY 3> OF Glu Ser Val Phe 50	aaa caa caa caa caa caa caa caa caa caa	gtatt atgta aaacg atctg aaata O NO: H: 48 PRT SSM: JCE: Arg Thr 20 Arg Gly	ttcta actorized gtatorized gatgorized actatorized acta	aa	ataaa agcac cctgg agtto cctto Gly Lys Arg Val 55	egicu Ala Trp 40 Ser Asn	c ace the ggt c ccc gte Thr Gly 25 Phe Ala	Ala 10 Leu Ala Asn Leu	Val Gln Thr Val Ile	Glu Ala Val Leu 60 Ser	Gln Thr Val 45 Gly Ser	His Ser 30 Leu Pro	Leu 15 Ser Asn Thr	Leu Asp Ala Phe Glu 80	1852 1912 1972 2032 2092 2152			
166 168 170 172 174 176 180 181 182 184 185 186 189 191 192 194 195 197 198 200	ggaa tgag aaat actg ctgt taca <210 <211 <212 <400 Met 1 Gln Ala Pro 65 Ile	aagaa gagat tagtt tagtt gctct taatcaa 0> SE 1> LE 2> TY 3> OF 0> SF Glu Ser Val Phe 50 Asp	aaa caaa caat aat aat aac aat aac aac aa	tatter at the state of the stat	tttta actig gtatig ggtco gatg actati 2 Ratt 2 Gly Fro Thr Met Arg 85	aa	ataaa agcac cctgg agtto cctto Orve Gly Lys Arg Val 55 Val	egicu Ala Trp 40 Ser Asn	c ace the ggt control graph of the ggt control graph of the graph of t	Ala 10 Leu Asn Leu 90	Val Gln Thr Val Ile 75 Gly	Glu Ala Val Leu 60 Ser	Gln Thr Val 45 Gly Ser	His Ser 30 Leu Pro	Leu 15 Ser Asn Thr Ser Val 95	Leu Asp Ala Phe Glu 80 Gly	1852 1912 1972 2032 2092 2152			

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\06222005\J539032.raw

204				100					105					110		
204	II.	T 011	T 011		77-	77.	C1	T 011		T 011		Dwa	Dho		T	Thr
	His	ьеu		TIIL	AIA	Ala	GIY		TAT	теп	TIII	PIO		Cys	пуs	1111
207			115	_				120	_			~1	125	_	-1	<b>~</b> 1
	Ala		ьeu	Leu	Thr	Ala		Met	ser	тте	Thr	_	vaı	ser	Pne	GIA
210	_	130			_	_	135	_				140				
212	Val	Leu	Asp	Thr	Gly	_	Asn	Val	Leu	Ile		Asp	Leu	$\mathtt{Trp}$	Gly	Asp
	145					150					155					160
215	Lys	Gly	Ala	Pro	His	Ile	Gln	Ala	Leu	His	Phe	Ser	Phe	Ala	Leu	Gly
216					165					170					175	
218	Ala	Phe	Leu	Ala	Pro	Leu	Leu	Ala	Lys	Leu	Ala	Trp	Gly	Thr	Thr	Ala
219				180					185					190		
221	Ser	Ala	Gln	Asn	His	Thr	Glu	Pro	Gln	Leu	Asp	Arg	Ser	Ala	Leu	Asn
222			195					200					205			
224	Arg	Ser	Phe	Glu	Ala	Ala	Ser	Asp	Ser	Val	Leu	Ala	Val	Pro	Asp	Asp
225		210					215					220				
227	Met	Asn	Leu	Leu	Trp	Ala	Tyr	Ala	Ser	Ile	Gly	Thr	Tyr	Val	Leu	Val
	225				-	230	-				235		-			240
230	Leu	Ser	Val	Phe	Leu	Phe	Ala	Pro	Phe	Phe	Lys	Lys	Arq	Ser	Lys	Gln
231					245					250	•	-			255	
	Lys	Lvs	Ser	Ala	Ala	Ser	Ala	Gln	Glv	Ala	Ara	Ara	Ala	Lvs	Tvr	His
234				260					265					270	-1-	
	Arg	Ala	Leu		Cvs	Leu	Leu	Phe		Phe	Phe	Phe	Phe		Val	Glv
237			275		-7-			280					285	-1-		V-1
	Ala	Glu		Thr	Tvr	Glv	Ser		Val	Phe	Ser	Phe		Thr	Thr	His
240		290			-1-	<b>U</b> -1	295	-1-				300				
	Val		Met	G] 11	Glu	Ser		Δla	Δla	Glv	T.e11		Ser	Tle	Phe	מידו
	305	<b>0-</b> 1			014	310	<u></u>			011	315		501			320
	Gly	Thr	Dhe	Δla	Δla		Δra	G1 17	T.011	Δla		Dhe	Dhe	Δla	Thr	
246	O-1			1114	325	Cyb	****9	017	шси	330	110	1110	1110	1114	335	Deu
	Leu	Gln	Dro	G1 17		Mο+	Mot	Tall	T.011		Acn	Tla	Gl v	Ser		Δla
249	пси	OIII	110	340	1111	ricc	ricc	vai	345	Cys	Abii	110	OLY	350	пси	nia
	Ser	Sar	Dhe		T.011	1721	T.011	Dhe		Lare	Car	Dro	T.011		T.011	Trn
252	Del	Der	355	FIIC	пец	Val	пец	360	дар	цуз	Ser	FIO	365	Cys	пец	110
	Ile	λla		Cor	17a l	Пала	Clv		Cor	Mot	ת ד ת	ת ד ת		Dho	Dro	Sor
255	116	370	SET	SCI	vai	TYL	375	AIA	DET	Mec	Ala	380	1111	FIIC	PLO	per
	C1		C0~	m~~	T10	C1.,		The second	The	mh~	T 011		C3	T	C0*	71-
258	Gly	TIE	ser	пр	116	390	GIII	TAT	TIIL	1111	395	TIII	GIY	пув	ser	400
		Dha	т1а	T 0	77.7		77.	77-	T 011	<b>~1</b>		Mob	77-	mb	Dwa	
	Ala	Pne	TIE	ьeu		GIY	Ата	Ala	neu	_	Leu	Met	Ala	TILL		Ala
261	T	0	<b>a</b> 1	<b>-</b> 1-	405	<b>~1</b>	<b>~1</b>	774	m	410	7	<b>T</b>	D	77-7	415	T
	Leu	ser	GIY		ьeu	GIN	GIY	HIS		Pro	Asp	ьeu	Pro		тте	Leu
264	_		_	420		_			425				_	430	_	
	Tyr	Met	_	ьeu	GIY	ser	Ala		Leu	Thr	Thr	Val		Pne	Pro	Val
267		_	435					440	_	_			445			_
	Met	_	Lys	Val	Ala	Thr		Pro	Leu	Asp	Arg		GIn	Glu	Lys	Ser
270		450	_				455				_	460				
	Ile	Asn	Ser	Glu	Gly		Lys	Ile	Leu	Leu		Ser	Ser	Arg	Leu	
273						470					475					480
	Lys			_												
279	<210	)> SE	EQ II	ON C	: 3											

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\06222005\J539032.raw

280 <211> LENGTH: 20 281 <212> TYPE: DNA 282 <213> ORGANISM: Artificial Sequence 284 <220> FEATURE: 285 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-1 forward 286 primer 288 <400> SEQUENCE: 3 289 tcggaaatgg agttccgtgg 20 292 <210> SEQ ID NO: 4 293 <211> LENGTH: 22 294 <212> TYPE: DNA 295 <213> ORGANISM: Artificial Sequence 297 <220> FEATURE: 298 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-2 forward 299 primer 301 <400> SEQUENCE: 4 302 agctgcctta ctgactgcca tg 22 305 <210> SEQ ID NO: 5 306 <211> LENGTH: 21 307 <212> TYPE: DNA 308 <213> ORGANISM: Artificial Sequence 310 <220> FEATURE: 311 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-3 forward 312 primer 314 <400> SEQUENCE: 5 21 315 tacgtattct ccttcgccac c 318 <210> SEQ ID NO: 6 319 <211> LENGTH: 21 320 <212> TYPE: DNA 321 <213> ORGANISM: Artificial Sequence 323 <220> FEATURE: 324 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-4 forward primer 325 327 <400> SEQUENCE: 6 328 tgtgtaacat tggcagcctg g 21 331 <210> SEO ID NO: 7 332 <211> LENGTH: 20 333 <212> TYPE: DNA 334 <213> ORGANISM: Artificial Sequence 336 <220> FEATURE: 337 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-5 forward primer 340 <400> SEQUENCE: 7 341 taacccatag ctgaggtctc 20 344 <210> SEQ ID NO: 8 345 <211> LENGTH: 24 346 <212> TYPE: DNA 347 <213> ORGANISM: Artificial Sequence 349 <220> FEATURE:

VERIFICATION SUMMARY

DATE: 06/22/2005

PATENT APPLICATION: US/10/539,032

TIME: 10:30:28

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\06222005\J539032.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date